

**WHAT IS CLAIMED IS:**

1. A method for providing an internal standard for normalizing the relative  
5 intensities of signals on a hybridization array, comprising:  
  
adding a known quantity of an unlabelled ribosomal nucleic  
acid competitor probe into a hybridization buffer suitable for  
the array experiment, the competitor probe characterized in  
10 that it has the same as a portion of a capture probe present  
in the array for immobilizing ribosomal nucleic acids thereon;  
and  
  
allowing the competitor probe to compete with a ribosomal  
15 capture probe for hybridization to a suitably labelled rRNA-  
derived cDNA of a cDNA sample, such that a hybridization  
signal of labelled rRNA-derived cDNA is decreased to a  
suitable signal dynamic range of detection and the rRNA-  
derived cDNA of the sample becomes a suitable internal  
20 standard for the hybridization array.
2. A method for normalizing the relative intensities of signals on a  
hybridization array, comprising:  
  
25 reproducing the method of claim 1 with a first reference sample labelled  
with a first label, and with a second test sample labelled with a second  
label; and  
comparing the intensity of a hybridization signal of hybridized rRNA-  
derived cDNA originating from the test sample to the intensity of a  
30 hybridization signal of hybridized rRNA-derived cDNA originating from  
the reference sample, to obtain a normalization factor.
3. A hybridization assay comprising:  
reproducing the method of claim 2; and  
35 normalizing the signals provided for each label for a given  
target nucleic acid hybridizing to a target-specific capture  
probe, said target originating from the reference and being

labelled with the first label and from the test sample and being  
labelled with the second label, with the normalization factor.

4. A method as defined in any one of claims 1 to 3, further comprising:  
5 determining the quantity of hybridized rRNA-derived cDNA.
5. A method as defined in claim 4, further comprising:  
10 comparing the quantity of hybridized rRNA-derived cDNA  
against standard curves to determine the quantity of cDNA in  
said sample.
6. A method as described in any one of claims 1 to 5, wherein said rRNA  
15 competitor probe is present in a concentration that is about 5 to about  
100 times that of the rRNA-cDNA probe.
7. A method as described in anyone of claims 1 to 6, wherein said rRNA-  
20 derived cDNA is labelled by 3' addition of phosphate, cyanines, biotin,  
digoxigenin, fluorescein, a dideoxynucleotide, an amine, a thiol, an azo  
(N<sub>3</sub>) group, fluorine, or any other form of label.
8. A method as described in any one of claims 1 to 7, which is used in high-  
25 throughput screening.
9. A method as described in any one of claims 1 to 8, wherein said array  
experiment consists in the identification of sequences found in the open  
reading frame of genes coding for transcription factors.
- 30 10. A method as described in claim 8, wherein said transcription factors  
include c-Rel, E2F-1, Egr-1, ER, NFκB p50, p53, Sp1 and YY1.
11. A solid support displaying an array of probes bound thereto, which array  
35 comprises a capture probe complementary to ribosomal nucleic acids or  
to cDNA derived therefrom.

12. A hybridization kit which comprises the solid support of claim 11 and, as a separate component, a competitor probe, the sequence of which comprises a least a portion of the sequence of the capture probe.